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"Developmental biochemistry of cottonseed embryogenesis and germination. XVIII. cDNA and amino acid sequences of the men the storage protein families.";
Plant Mol. Biol. 7:475-489(1986).
-i- FUNCTION: SEED STORAGE PROTEIN.
-i- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOI
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                                                                                              GLB1_MAIZE STANDARD; PRT; 573 AA. P15590; Ol-APR-1990 (Rel. 14, Created) Ol-AUG-1990 (Rel. 15, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) GLOBULIN-1 S ALLELE PRECURSOR (GLB1-S) (7S-LIKE).
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HSSP;
                           SEQUENCE FROM N.A.
                                                             Zea mays (Maize).
Eukaryota; Viridiplantae;
                                                                                        GLB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO; IPR001113; -. PFAM; PF00546; Seedstore_7s;
                                                  Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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; P50477; 1CAX.
                                                                                                                                                                                                                                                                                          KRHEEEEDV-----HYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLFAFG-----I
                                                                                                                                                                                                                                                                                                                                                                            GMFRKASQEQIRALSQEATSPR----EKSGE--RFAFULLYRTPRYSNQNGRFYEACPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTEYLINRDNNERLHIAKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEDCRRRCEQQE -- PRQQYQCQRRCREQQRQHGRGGDLINPQR-----GGSGRYEEGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R--QQEERQRPQCQQRCLKRFEQEQQQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDPQTDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQYEQCQERC
                                                                                                                                                                                                                           NPDHNQRIFVAGKINHV-RQWDSQAKELAFGVSSRLVDEIFNNNPQESYFVS-RQRQRAS
                                                                                                                                                                                                                                                                             EQQQEQEQEEERRSGQYRKIRSQLSRGDIFVVPANFPVTFVASQNQNLRMTGFGLYNQNI
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 INBRED LINE VA26; .C., Kriz A.L.;
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69729 MW;
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                                                             Embryophyta; Tracheophyta;
                                                  Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1083.5;
Pred. No. 8.7
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                                                  Poaceae;
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                                                              Spermatophyta;
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Query Match
Best Local S
Matches 203
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00546; Seedstore_7s; 1.
Seed storage protein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *Characterization of embryo globulins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
POLYMORPHISM: THE THREE MOST COMMONIX OCCURRING GLB1 ALLELES ITHE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS, RESPECTIVELY
                                                                                                                                                                                       LYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEDNKRDPQQREYEDCRRRCEQQEPRQQYQCQRRCRE-----QQRQHGRGGDLINPQRG
                       VVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEELFN
                                                                  IVCPHRQSQGGESERERGKGRRSEEEEESSEEQEEVGQGYHTIRARLSPGTAFVVPAGHP
                                                                                                             MACPHLSGRHG----GRRGGKRHEEEEDVHYEQ-----VKARLSKREAIVVPVGHP
                                                                                                                                                          SIANQHGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLYNTRSFKIAYVPNGKGYAE
                                                                                                                                                                                                                                                     RLERLFGRHGQDKGIIVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRP
                                                                                                                                                                                                                                                                             RLRGVLGQ--QREGVIISASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLFNKRP
                                                                                                                                                                                                                                                                                                                                                VTYLANTDGRKKLVITKILHTISVPGEFQFFFGPGGRNPESFLSSFSKSIQRAAYKTSSD
                                                                                                                                                                                                                                                                                                                                                                   TFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                   DYRVAVLEANPRSFVVPSHTDAHCIGYVAEGEGVVTTIENGERRSYTIKQGHVFVAPAGA 199
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P50477; 1CAW.
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Physiol. 91:636-643(1989).
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573 AA;
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39.9%;
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Pred. No. 1.9e
84; Mismatches
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hes 180;
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Burks A.W., Cockrell G., Stanley J.S., Helm R.M., Bannon G.A.;
"Recombinant peanut allergen Ara h I expression and IgE binding patients with peanut hypersensitivity.";
J. Clin. Invest. 96:1715-1721(1995).
-!- SIMILARITY: TO 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arachis hypogaea (Peanut).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; eudicoty; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _ARAHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L38853; AAA60336.1; HSSP; P50477; 1CAW.
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FSRNTLEAAFNAEFNEIRRVLLEENAGGEQEERGQRRRSTRSSDNEGVIVKVSKEHVQEL
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(Rel. 32, Last sequence up
(Rel. 35, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                        EMBL; M13759; AAB01374.1; EMBL; J01290; -; NOT_ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-83143289; PubMed-6897678;
Schuler M.A., Ladin B.F., Pollaco J.C., Freyer G., Beach
"Structural sequences are conserved in the genes coding
alpha, alpha' and beta-subunits of the soybean 7S seed s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=86250867; PubMed=3013879;
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sj
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Fabales; Fabaceae; Papilionoideae; Glycine.
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01-OCT-1989 (Rel. 12, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
BETA-CONGLYCININ, ALPHA' CHAIN PRECURSOR.
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                                                                                                                                                    tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leic Acids Res. 10:8245-8261(1982).

FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING. SUBUNIT: THE ALPHA'-, ALPHA-, AND BETA-SUBUNIT'S ASSOCIATE I VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.

VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.

SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR
      B24810; I
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"Recombinant peanut allergen Ara h I expression and 1gE binding
patients with peanut hypersensitivity.";
J. Clin. Invest. 96:1715-1721(1995).
-i- SIMILARITY: TO 75 SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
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the European Bioinformatics Institute. The
use by non-profit institutions as long a
modified and this statement is not removed.
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MEDLINE=96013631; PubMed=7560062;
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Eukaryota; Viridiplantae;
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CARBOHYD
SEQUENCE
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Seed storage protein; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED
DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE A
CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.
-!- SUBUNIT: THE ALPHA -, ALPHA -, AND BETA-SUBUNITS ASSOCIATE IN
VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
-!- SUBCELLULAR LOCATION: EMBRYO AXIS, AND COTYLEDONARY MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLCA_SOYBN P13916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.).
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37, Last annotation update)
ALPHA CHAIN PRECURSOR.
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    Glycoprotein; Multigene family.

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Pred.
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N-LINKED (GLCANC. . .) (POTENTIAL).
N-LINKED (GLCANC. . .) (POTENTIAL).
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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-CV. FELTHAM FIRST;
MEDLINE-88326208; PubMed=3415641;
Bown D. Ellis T.H.N., Gatehouse J.A.;
"The sequence of a gene encoding conviciling the sequence of a gene encoding t
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01-JAN-1990 (Rel. 13; Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
CONVICILIN PRECURSOR.
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
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SBP_SOYBN
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Best Local Similarity 32.7
Glycine max (Soybean).
Bukaryota; Viridiplantae; Embryophy
Magnoliophyta; eudicotyledons; core
Fabales; Fabaceae; Papilionoideae;
                                                              SBP_SOYBN STANDARD; PRT; 524 AA Q04672; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 01-JUN-1994 (Rel. 29, Last annotation update) SUCROSE-BINDING PROTEIN PRECURSOR (SBP).
                                                     SBP.
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PFAM; PF00546; Seedstore_7s;
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PIR; S00566; S00566
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                                                                                                                                                                                                                                                                                                                                                   GKLFEITPEKKYPQLQDLDILVSCVEINKGALMLPHYNSRAIVVLLVNEGKGNLELL---
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                                                                                                                                                                                              PEQKEEESQR - - - KRSPLSSVLD
                                                                                                                                                                                                                       PROHOOOSSRSTKOOOPLVSILD
                                                                                                                                                                                                                                                                                                                     LSGRHGGRRGGKRHEEEE------DVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENL
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                                                                                                                                                                                                                                                L--GFGINAKNNQRNFLSGSDDNVISQIENPVKELTFPGSSQEVNRLIKNQKQSHFASAE
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              Embryophyta; Tracheophyta; Spermatophyta;
lons; core eudicots; Rosidae; eurosids I;
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Pred. No. 2.
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 Glycine
             eudicots;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
-I- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORY, INCLUDING THE
MESOPHYLL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF
MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.
-I- DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED
UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A 62-kD sucrose binding protein is expressed and tissues actively engaged in sucrose transport."; plant Cell 4:1561-1574(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00546; Seedstore_7s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; JQ1730; JQ1730.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grimes H.D., Overvoorde P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93104680; PubMed=1467654;
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SEQUENCE FROM N.A., AND SEQUENCE OF
     518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30 DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collab een the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                        KRPLYSNKYGQAYEVKPEDYRQ--LQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASG
                                                                                                                                                                           HIPAGTPLYIVNRDENDKLFLAMLHIPVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQ
                                                                                                                                                                                                             RIPAGTTFYLINRDNNERLHIA--KFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILE
                                                                                                                                                                                                                                                                             LLRALKNYRLVLLEANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVI 341
                                                                                                                                                                                                                                                                                                                                                    HGRGGDLINPQRGGSGRYEEGEEKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSK 281
                                                                                                                                                                                                                                                                                                                                                                                                                    KRYEEQQREDEEKYEERMKEEDNKRDPQQREYEDCKRRCEQQEPRQQYQCQRRCREQQRQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCKETEVEEE-----DPELVTCKHQCQQQQQYTEGDKR---VCLQSCD-RYHRMKQERE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCKEICEEEEEYNRQRDPQ--QQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQ 162
EADVEMACPHLSGRHGGRRGGKRHEEEEDVHYEQVKARLSKREATVVPVGHPVVFVSSGN
                                  KRPTISNGYGRLTEVGPDDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALVIDG
                                                                                                       AALQTPKGKLENVFDQQNEGSIFRISREQVRALA-PTKKSSWWPF--GGE-SKPQFNIFS
                                                                                                                                        AALNTQAERLRGVLGQQREGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFN
                                                                                                                                                                                                                                                LLQGIENFRLAILEARAHTFVSPRHFDSEVVFFNIKGRAVLGLVSESETEKITLEPGDMI
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524 AA;
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60522 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 798;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUCROSE-BINDING
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ein is expressed and localized in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0251EE90796EF341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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.9e-42;
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01-APR-1990 (Rel. 1
15-JUL-1999 (Rel. 3
  CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                             Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gatehouse J.A., Wright D.J., Boulter D.; "Isolation and expression of a pea vicilin cDNA in the yeast Saccharomyces cerevisiae."; Biochem. J. 251:857-864(1988).
                                                                                                              SIGNAL
                                                                                                                                                                 INTERPRO; IPR001113; -
PFAM; PF00546; Seedstore_7s; 1.
                                                                                                                                                                                                                                              EMBL; X14076; CAA32239.1; -.
EMBL; Y00722; CAA68708.1; -.
PIR; S00567; S00567.
PIR; S08505; S08505.
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Eukaryota; Viridiplantae; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Higgins T.J.V., Newbigin E.J., "The sequence of a pea vicilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THERE ARE AT LEAST 11 GENES FOR VICILIN SUBUNITS. SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILI CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
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                                                                                                                                     storage protein; Multigene family; Signal
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V -> L (IN REF. 2).
I -> V (IN REF. 2).
; E2FA390B95451D29
                                                                                     VICILIN.
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Query Match Best Local Similarity Matches 161;

21.5%;

Score 760.5; DE Pred. No. 5e-40;

DB 1; 159;

Length Indels

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Conservative

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P25974;
01-MAY-1992
                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contential modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max (Soybean).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                           processes.";
Plant Cell 1:415-425(1989)
                                                                                                                                                                                                                                                                                                                                            Harada J.J., Barker S.J., Goldberg R.B.;
"Soybean beta-conglycinin genes are clustered in several DNA and are regulated by transcriptional and posttranscriptional
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93005638;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                send
                                                                                                                                                                                     FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTEC GERMINATION TO PROVIDE CARBON AND NITRGESN SOURCE FOR THE DEVELOPING SEEDLING. SUBUNIT: THE ALPHA'-, ALPHA-, AND BETA-SUBUNITS ASSOCIATE I VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS. SUBCELLULAR LOCATION: EMBRRYO AXIS, AND COTYLEDONARY MEMBRAN VACUOLAR PROTEIN BODIES.
                                                                                                                                                    SIMILARITY: TO OTHER 7S SEED ST CONVICILIN, CONGLYCININ, ETC.).
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              requires a license agreement (See http://www.isb-sib an email to license@isb-sib.ch).
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RESULT 12
VCL_VICFA
ID VCL_VICFA
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Best Local Similarity
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01-AUG-1988 (Rel. (
01-AUG-1988 (Rel. (
01-JAN-1990 (Rel. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
CARBOHYD
SEQUENCE
                                                                                                                                            Vicia faba (Broad bean).
Eukaryota; Viridiplantae; Embryophyt
Magnoliophyta; eudicotyledons; core
           SEQUENCE FROM
                                              gene
                                                                     MEDLINE=88096511; Publ
Weschke W., Baeumlein
                                                                                             STRAIN=CV. MINOR;
                                                                                                                                                                                VICILIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seed storage protein;
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PFAM; PF00546; Seedstore_7s; 1
                                   Nucleic
                                                        "Nucleotide sequence
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                  Fabales;
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PIR; JQ0969; 1
                                                                                                                                                                                                                                                                                                      431 FPSIL
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                                                                                                                                                                                                                                                                                                                                                                                                                 GGKRHEEEEEDVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLEAFGINAQNNHENF
                                                                                                                                                                                                                                                                                                                                                      LAGEKDNVVRQIERQVQELAFPGSAQDVERLLKKQRESYFVDAQPQQKEEGSKGRK--GP
                                                                                                                                                                                                                                                                                                                                                                           LAGRERNVLQQIEPQAMELAFAAPRKEVEELFNSQDESTFFPGPRQHQQQSSRSTKQQQP
                                                                                                                                                                                                                                                                                                                                                                                                   QQKQKQEEEPLEVQRYRAELSEDDVFVIPAAYP--FVVNATSNLNFLAFGINAENNQRNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPQLRDLDIFLSSVDINEGALLLPHFNSKAIVILVINEGDANTELV------GIKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVIVELSKEQIRQLSRRAKSSSRKTI----SSEDEPFNLRSRNPIYSNNFGKFFEITPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVIISASQEQIRELTRODSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVL-----GQQRE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQSDNPYYF-DERSLSTRERTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRIIGG--RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HHADADFLLFVLSGRAILTLVNNDDRDSYNLHPGDAQRIPAGTTYYLVNPHDHQNLKIIK 147
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                                  Acids Res.
                                                                                                                                Fabaceae;
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26
351
439
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13,
                                                                                PubMed=3697075;
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25 P
439 B
351 N
                                  15:10065-10065(1987)
                                                                                                                                  Papilionoideae;
                                                        n H., Wobus U.; ·
of a field bean (Vicia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.28;
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                                                                                                                                                                                                                     Created)
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                                                                                                                                             Embryophyta; Tracheophyta; Spermatophyta;
dons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                             sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 748; DB 1;
Pred. No. 2.8e-39;
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N-LINKED (GLCNAC: ..) (P
DBD8AA2A0776088B CRC64;
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                                                                                                                                                                                                                                              PRT;
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                                                                                                                               Vicia.
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                                                        L.var.minor)
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                                                          vicilin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y00506; CAA68559.1; -.
EMBL; Y00462; CAA68525.1; -.
PIR; S06309; S06309.
PIR; A27288; A27288.
HSSP; P50477; ICAW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removentities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88067789; PubMed=3684610; Bassuener R., van Nong H., Jung R., Saalbach G., Muentz K.; Bassuener R. van Nong H., Jung R., Saalbach G., Muentz K.; "The primary structure of the predominating vicilin storage protein subunit from field bean seeds (Vicia faba L. var. minor cv. Fribo)."; Nucleic Acids Res. 15:9609-9609(1987).
-i- FUNCTION: SEED STORAGE PROTEIN.
-i- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR001113; -
PFAM; PF00546; Seedstore_7s; 1.
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nes 157; Conserv
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SIMILARITY: TO OTHER 7S SEED ST.
CONVICILIN, CONGLYCININ, ETC.).
ERERGSQEIKDH--LYSIL 460
                                                                                                                                                                                                        QAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLS
                                                                                                                                                                                                                                               DRRQRGQEENVIVKISRKQIEELNKNAKSSS----KKSTSSESEPFNLRSREPIYSNKFG
                             HQQQSSRSTKQQQPLVSIL 661
                                                                                     FAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEELFNSQDESIFFPGPRQ
                                                                                                                       NQQGLR----EEYDEEKEQGEEEIRKQVQNYKAKLSPGDVLVIPAGYPVAIKASSNLNLV-
                                                                                                                                                    GRHGGRRGGKRHEEEEDVHYEQV-----
                                                                                                                                                                                   KFFEITPKRNPQLQDLNIFVNYVEINEGSLLLPHYNSRAIVIVTVNEGKGDFELVGQRNE
                                                                                                                                                                                                                                                                                                            VNRPGEPQSFLLSGNQNQPSILSGFSKNILEASFNTDYKEIEKVLLEEHGKEKYHRRGLK 212
                                                                                                                                                                                                                                                                                                                                           ISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVLGQ-------
                                                                                                                                                                                                                                                                                                                                                                        ADFILVVLSGKAILTVLLPNDRNSFSLERGDTIKLPAGTIGYLVNRDDEEDLRVLDLVIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DNPFVFESNRFQTLFENENGHIRLLQKFDQHSKLLENLQNYRLLEYKSKPHTIFLPQQTD
                                                           -GFGINAENNQRYFLAGEEDNVISQIHKPVKELAFPGSAQEVDTLLENQKQSHFANAQPR
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443
463 AA;
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257
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52694 MW;
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R -> K (IN REF.

R -> Q (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 711.5; DB 1; Pred. No. 5.2e-37;
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                                                                                                                                       -KARLSKREAIVVPVGHPVVFVSSGNENLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22)
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RESULT 13 VCLB_PEA

RESULT 14
CANA_CANEN
ID CANA_C

CANA_CANEN

STANDARD;

PRT;

445

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Best Local Similarity
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The vicilin gene family of pea (Pisum sativum L.): a complete cDNA coding sequence for preprovicilin.";
Nucleic Acids Res. 11:2367-2380(1983).
-!- FUNCTION: SEED STORAGE PROTEIN.
-!- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (CLONES PDUB7 STRAIN=CV. FELTHAM FIRST; MEDLINE=83220791; PubMed=6687941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROVICILIN PRECURSOR (TYPE B) (FRAGMENT).
Pisum sativum (Garden pea).
Eukaryota, Viridiplantae; Embryophyta; Tri
Magnoliophyta; eudicotyledons; core eudico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VCLB_PEA STANDARD; PRT; 4
P02854;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
01-JAN-1990 (Rel. 13, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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PIR; A03344; FWPMVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: TO OTHER 7S CONVICILIN, CONGLYCININ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boulter D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fabales; Fabaceae; Papilionoideae;
372
                                                                                                                                                                                                                                                     470
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                                                                                              314
                                                                                                                                                                                                                                                                                                                                                                                                     140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 DNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPTHLD : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                       200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BODIES
                                                                                           ; PF00546; Seedstore_7s; 1. storage protein; Glycoprotein; Multigene
                                                                                                                                                                                              KFFEITPEKNQQLQDLDIFVNSVDIKVGSLLLPNYNSRAIVIVTVTEGKGDFELVGQR--
                                                                                                                                                                                                                                             QAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLS
                                                                                                                                                                                                                                                                                                  DRRQEINEENVIVKVSRDQIEELSKNAKSSS----KKSVSSESGPFNLRSRNPIYSNKFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENPFIFKSNRFQTLYENENGHIRLLQKFDKRSKIFENLQNYRLLEYKSKPHTLFLPQYTD
                                            NAQNNHENFLAGRERNVLQQTEPQAMELAFAAPRKEVE
                                                                                                                                                                                                                                                                                                                                                                                                                               ADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQT
NAENNERNFLAGEEDNVTSQVERPVKELAFPGSSHEVD
                                                                                                                                                                                                                                                                                                                                              -----EGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYG
                                                                                                                                                                                                                                                                                                                                                                                                     VNKPGQLQSFLLSGTQNQKSSLSGFSKNILEAAFNTNYEEIEKVLLEQQEQEPQHRRSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADFTLVVLSGKATLTVLKSNDRNSFNLERGDAIKLPAGSIAYFANRDDNEEPRVLDLAIP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P50477; 1.CAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410
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221
359
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>410
222
359
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37.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Embryophyta; Tracheophyta; Spermatophyta; dons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEED STORAGE
, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gatehouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 704.5;
Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROVICILIN.
CLEAVAGE (POTENTIAL).
N-LINKED (GLCNAC. . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8AF68CE85A316FA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; DB 1;
1.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEINS (PHASEOLIN, VICILIN,
409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilroy J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Croy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                   469
                                                                                                                                                                                                                                                                                                                                                                                                     199
                                                                                                                                             587
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X59467; CAA42075.1; -.
PDB; ICAU; 31-OCT-93.
PDB; ICAW; 31-OCT-93.
PDB; ICAW; 31-OCT-93.
PDB; ICAW; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ng J.D., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P50477;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94143476; PubMed=8310056;
KO T. P., Ng J.D., McPherson A.;
"The three-dimensional structure of canavalin from (Canavalia ensiformis).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ng J.D., Stinchcombe T., Ko T.-P., Alexander E., M

"PCR cloning of the full-length cDNA for the seed

from the jack bean plant, Canavalis ensiformis.",

Plant Mol. Biol. 18:147-149(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canavalia ensiformis (Jack bean) (Horse bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sy
Magnoliophyta; eudicotyjedons; core_eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seed storage protein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=COTYLEDON;
MEDLINE=92119225; PubMed=1731967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CANAVALIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00546; Seedstore_7s; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ensiformis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94143475; PubMed=8310055; Ng J.D., Ko T.-P., McPherson A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=COTYLEDON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [NTERPRO;
     152
                                                                                                                                                            295
                                                                                                         92
                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                               32
DNNQNLRILKFAITFRRPGTVEDFFLSSTKRLPSYLSAFSKNFLEASYDSPYDEIEQTLL
                                                   DNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERL-RGVL
                                                                                                   CSKPNTLLLPHHSDSDLLVLVLEGQAILVLVNPDGRDTYKLDQGDAIKIQAGTPFYLINP
                                                                                                                              EANPNAFVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINR 354
                                                                                                                                                                                                                                                          GGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLL
                                                                                                                                                                                                          GGEAEDESEESRAQNNPYLFRSNKFLTLFKNQHGSLRLLQRFNEDTEKLENLRDYRVLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression, and crystallization s) canavalin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001113; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
445 AA;
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101:713-728(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445
                                                                                                                                                                                                                                                                                                                                                                                                                                                    50326 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                           19.5%;
                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
CANAVALIN.
                                                                                                                                                                                                                                                                                                                                           Score 689.5; DB 1
Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30383C5F83A1E9B7 CRC64;
                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                   163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jack bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McPherson
                                                                                                                                                                                                                                                                                                                                                                   Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHASEOLIN, VICILIN
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein canavalin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Canavalia
                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Α.;
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                            91
  211
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RESULT 15
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P10562;
01-JUL-1989 (Rel. 1
01-JUL-1989 (Rel. 1
01-OCT-1996 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANAVALIN PRECURSOR.

Canavalia gladiata (Sword bean) (Japanese jack bean).

Cunavalia gladiata (Sword bean) (Japanese jack bean).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Embryophyta; Rosidae
                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Magnoliophyta; eudicotyledons; core eud
Fabales; Fabaceae: Panilionnia-
                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ewthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                    Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89296493; PubMed=2740227;
Takei Y., Yamauchi D., Minamikawa T.;
"Nucleotide sequence of the canavalin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamauchi D., Nakamura K., Asahi T., Minamikawa T.;
"CDNAs for canavalin and concanavalin A from Canavalia gladiata
seeds. Nucleotide sequence of cDNA for canavalin and RNA blot
analysis of canavalin and concanavalin A mRNAs in developing se
                SIGNAL
                                  Seed
                                             INTERPRO; IPRO01113; -.
PFAM; PF00546; Seedstore_7s;
                                                                            PIR; S00281; S00281.
HSSP; P50477; 1CAW.
                                                                                                         EMBL; X06733; CAA29910.1; -. EMBL; X15076; CAA33172.1; -.
                                                                                                                                                                                                                                                                                                                                                              seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88111636; PubMed=3338449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
                                                                                                                                                                                                                                                                                  SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                 FUNCTION:
              storage protein; Signal.
AL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biochem. 170:515-520(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRAHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKQQQP 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNERNFLAGHKENVIRQIPRQVSDLTFPGSGEEVEELLENQKESYFVDGQPRHIDAGGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEELFNSQDESIFFPGPRQHQQQSSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GLEQQQQQGLESMQLRRYAATLSEGDIIVIPSSFPVALKAASDLNMV--GIGVNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRRGGKRHEEEEDVHYEQVK---ARLSKREAIVVPVGHPVVFVSSGNENLLLFAFGINAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITPEKNSQLRDLDILLNCLQMNEGALFVPHYNSRATVILVANEGRAEVELV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEEQEGVIVKMPKDQIQEISKHAQSSSRKTL----SSQDKPFNLRSRDPIYSNNYGKLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQQREGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYE
                                                                                                                                                                                                       non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                 Res. 17:4381-4381(1989).
SEED STORAGE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11, Created)
11, Last sequence up
34, Last annotation
CANAVALIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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